

What is claimed is:

- A nucleic acid probe array comprising a set of probes for interrogating the
 joining sequence between a first sequence element and a second sequence
 element.
- 5 2. The probe array of Claim 1 wherein said nucleic acid is oligonucleotide.
 - 3. The probe array of Claim 1 wherein said first sequence element is a first exon and said second sequence element is a second exon.
 - 4. The probe array of Claim 3 wherein said joining sequence is the 3' sequence of said first exon and 5' sequence of said second exon.
- 10 5. The probe array of Claim 4 wherein said joining sequence is at least 20 bases.
 - 6. The probe array of Claim 5 wherein said joining sequence is at least 30 bases.
 - 7. The probe array of Claim 6 wherein said joining sequence is at least 40 bases.
 - 8. The probe array of Claim 7 wherein said joining sequence is at least 50 bases.
 - 9. The probe array of Claim 8 wherein said joining sequence is at least 100 bases.
 - 10. The probe array of Claim 1 wherein said set of probes are immobilized on a substrate at a density of at least 100 probes/cm².
 - 11. A method for determining target sequence wherein said target sequence comprises a first sequence element joining a second sequence element comprising:
- a) hybridizing said target sequence with a nucleic acid probe array comprising a set of probes for interrogating the joining sequence between said first sequence element and said second sequence element; and
 - b) obtaining information about the joining sequence based upon the

- 12. The method of Claim 11 wherein said first and second sequence elements are exons.
- 13. The method of Claim 12 wherein said set of nucleic acid probes are oligonucleotide probes.

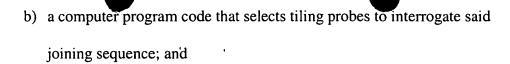
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- 14. The method of Claim 13 wherein said set of nucleic acid probes are immobilized on a substrate.
- 15. The method of Claim 14 wherein said set of nucleic acid probes are immobilized at a density of at least 100 probes/cm².
- 10 16. The method of Claim 12 wherein said target sequence is a mRNA.
 - 17. The method of Claim 16 wherein said mRNA is one of at least two alternatively spliced mRNAs transcribed from a gene.
 - 18. The method of Claim 11 further comprising the step of quantifying said first and second sequence elements using said information about the joining sequence and said hybridization.
 - 19. The method of Claim_11 wherein said nucleic acid probe array comprising sequence probes against said first and second sequence elements.
 - 20. The method of Claim 19 further comprising quantifying said first and second sequence elements based upon the hybridization of said target sequence and said sequence probes.
 - 21. The method of Claim 11 wherein said probes for interrogating are probes for tiling said joining sequence.
 - 22. The method of Claim 21 wherein said joining sequence is at least 20 bases.

- 23. The method of Claim 22 wherein said joining sequence is at least 30 bases.
- 24. The method of Claim 23 wherein said joining sequence is at least 40 bases.
- 25. The method of Claim 24 wherein said joining sequence is at least 50 bases.
- 26. The method of Claim 25 wherein said joining sequence is at least 100 bases.
- 5 27. The method of Claim 19 wherein said probes are oligonucleotides.
 - 28. A computer software product comprising:
 - a) Computer code that receives a plurality of hybridization signals, wherein each of said plurality of signals reflects the hybridization of one of plurality of tiling probes to interrogate the joining sequence of a target sequence wherein said target sequence has at least one sequence element that is selected from a group of at least two sequence elements;
 - b) Computer code that identifies said sequence element based upon said hybridization signals; and
 - c) A computer readable media that stores said codes.
 - 29. The computer software of Claim 28 wherein said tiling probes are oligonucleotides immobilized on a substrate.
 - 30. The computer software of Claim 29 wherein said tiling probes interrogate at least 20 bases.
 - 31. The computer software of Claim 29 wherein said tiling probes interrogate at least 30 bases.
 - 32. The computer software of Claim 29 wherein said tiling probes interrogate at least 40 bases.
 - 33. The computer software of Claim 29 wherein said tiling probes interrogate at



- 34. The computer software of Claim 29 wherein said tiling probes interrogate at least 100 bases.
- 35. The computer software of Claim 28 further comprising computer code that quantifies said target sequence.
- 36. A method for designing probes for detecting the combination of two sequence elements comprising:
 - a) inputting the sequence of the joining region between said two sequence elements; and
 - b) selecting probes for tiling the said joining region based upon said sequence.
- 37. The method of Claim 36 wherein said two sequence elements are exons.
- 38. The method of Claim 37 further comprising a step of designing lithographic mask wherein said lithographic mask is used in the fabrication of arrays of nucleic acid probes.
- 39. The method of Claim 38 further comprising a step of output signals for controlling an ink-jet printing mechanism for depositing compounds on a substrate.
- 40. The method of Claim 38 wherein said sequence is at least 20 bases.
- 41. The method of Claim 40 wherein said sequence is at least 30 bases.
- 42. The method of Claim 41 wherein said sequence is at least 40 bases.
- 20 43. The method of Claim 42 wherein said sequence is at least 50 bases.
 - 44. The method of Claim 43 wherein said sequence is at least 100 bases.
 - 45. A computer software product comprising:
 - a) a computer program code that constructs a joining sequence;



- c) a computer readable media that stores said codes.
- 46. The computer software product of Claim 45 wherein said joining sequence is for one of alternatively spliced mRNAs.
- 47. The computer software product of Claim 46 further comprising computer code that inputs exon sequences of one gene.
- 48. The computer software product of Claim 47 wherein said joining sequence is constructed based upon said exon sequences.
- 49. The computer software product of Claim 48 further comprising code that outputs sequence of said probes.